



Local Genetic Correlations

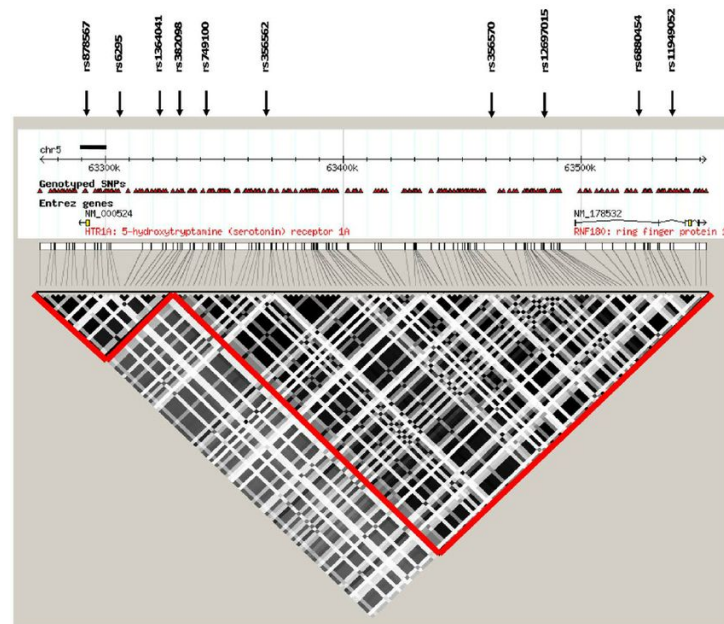
Data Science HK 2.12.2018

Genetic correlation - quick & dirty in one afternoon

- Hypothesis: mental disorders may share specific genes
- Methodology
 - GWAS - genome wide association study
 - Research data is split into LD blocks
 - “Linkage disequilibrium blocks” - chunks of human genes that are non-randomly associated
- Data sources
 - <https://www.med.unc.edu/pgc/results-and-downloads>
 - Psychiatric genomic consortium study result data sets
 - <https://raw.githubusercontent.com/tshmak/lassosum/master/inst/data/Berisa.EUR.hg38.bed>
 - LD block definitions

Base pair blocks

- 1600+ base pair blocks that contain chunks of associated base pairs
 - <https://raw.githubusercontent.com/tshmak/lassosum/master/inst/data/Berisa.EUR.hg38.bed>
 - Starting and ending points of each block as SNPs
 - Each block is given the chromosome it belongs to
- For each block and trait we can compute inflation factors
 - Inflation factor = strength of the signal
 - Inflation factor derived from the skewness of the distribution
 - Normal distribution = no signal
 - skewed distribution = signal



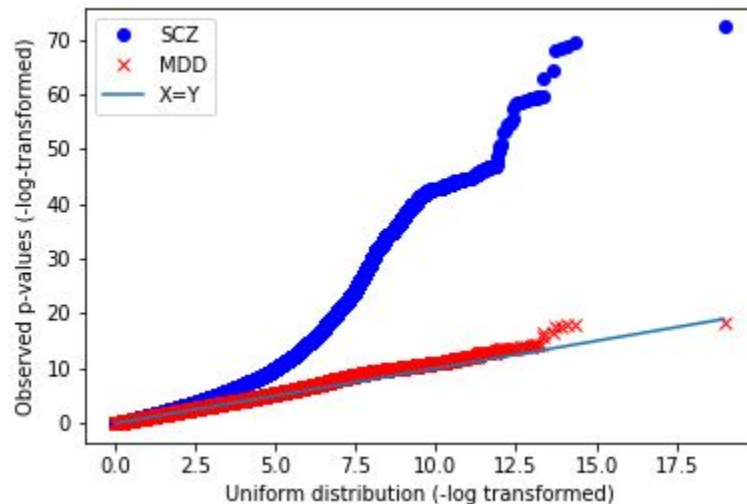
(Image for illustration purposes only
https://www.researchgate.net/figure/LD-plot-for-HTR1A-and-RNF180-LD-block-of-the-HTR1A-and-RNF180-regions-was-obtained-from_fig2_224915942)

BP blocks (first three rows)

chr	start	stop
chr1	1961168	3666172
chr1	3666172	4320751
chr1	4320751	5853833

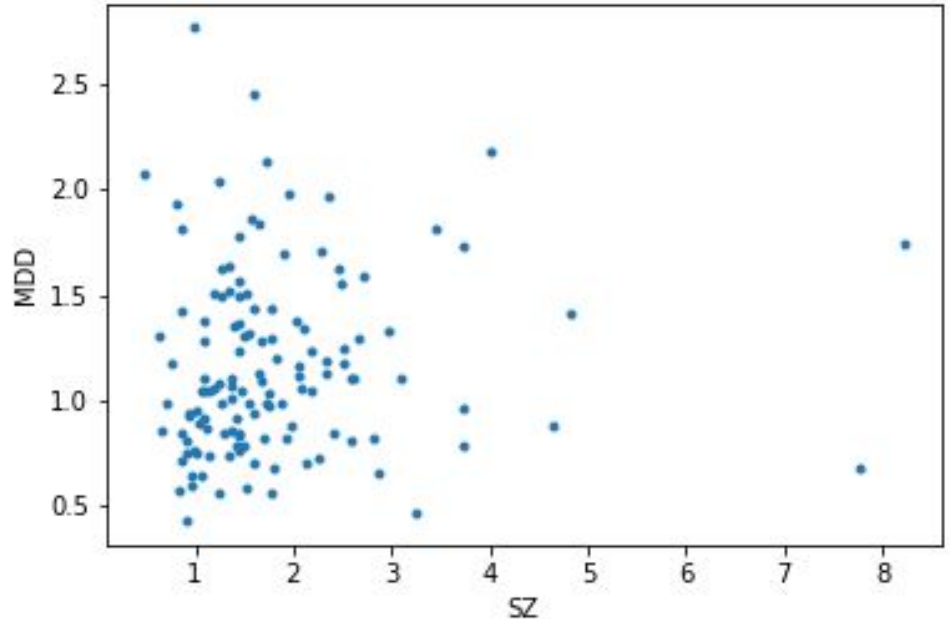
QQ-plot of p-values

- Diverting from the $X=Y$ indicates a signal: the p-values do not follow uniform distribution
- Conclusions from the QQ-plot:
 - Schizophrenia is more heritable and has more statistical power
 - Mdd does not
 - SCZ more narrowly described
 - MDDs description somewhat ambiguous



Signal strength in the first chromosome (chr1)

- There seems to be one LD-Block which has an effect in both SZ and MDD
- Most blocks are phenotype specific



Finally

Conclusions

- There seems to be some genomic region with shared effect
- A quick and dirty way to explore the overlap between these two phenotypes
- One can do a lot more on this (a whole PhD)

Caveats

- Computation power
- We did not investigate more than chromosome 1
- Sample used in both studies might overlap (the controls)
- We might have missed a number of things by reducing the problem to LD blocks only
- Inflation factors are not a good measurement